



SEQUENCE LISTING

<110> Brzostowicz, Patricia C.
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#6

<120> CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

<130> CL1903 US NA

<150> 60/229,907

<151> 2000-09-01

<150> 60/229,858

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<213> Methylomonas 16a

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Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn
 35 40 45

Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser
 50 55 60

Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly
 65 70 75 80

Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu
 85 90 95

Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr
 100 105 110

Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp
 115 120 125

Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile
 130 135 140

Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu
 145 150 155 160

Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu
 165 170 175

Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly
 180 185 190

Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val
 195 200 205

Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met
 210 215 220

Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg
 225 230 235 240

Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg
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Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met Ala Ile Asp
 260 265 270

Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp
 275 280 285

Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val
 290 295 300

Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly
 305 310 315 320

His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln
 325 330 335

Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly
 340 345 350

Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Met Arg Leu Ile
 355 360 365

Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser
370 375 380

Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile
385 390 395 400

Glu Phe Pro Arg Ile Lys Gly Gly Lys Pro Phe Asn Ile Asp Thr Asp
405 410 415

Trp Phe Asn Ser Met Leu Ser Glu Ile Gly Gln Pro Lys Gly Gly Lys
420 425 430

Val Glu Val Ser His
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<213> Methylobionas 16a

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<213> Methylobionas 16a

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20 25 30

Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu
35 40 45

Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val
50 55 60

Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu
65 70 75 80

Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile
85 90 95

Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu
100 105 110

Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly
115 120 125

Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro
130 135 140

Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro
145 150 155 160

Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys
165 170 175

Asn Val Ala Cys Val Gly Gly Ser Trp Met Ala Pro Ala Asp Leu Val
180 185 190

Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala
195 200 205

Ala Leu Lys Lys
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<213> Methylobionas 16a

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<212> PRT
<213> Methylobionas 16a

<400> 6

Met Lys Leu Thr Thr Asp Tyr Pro Leu Leu Lys Asn Ile His Thr Pro
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20 25 30

Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
35 40 45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
50 55 60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65 70 75 80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
85 90 95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
100 105 110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
115 120 125

Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
130 135 140

Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145 150 155 160

Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
165 170 175

Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
180 185 190

Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
 195 200 205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
 210 215 220

Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
 225 230 235 240

Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
 245 250 255

Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
 260 265 270

Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
 275 280 285

Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
 290 295 300

Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
 305 310 315 320

Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
 325 330 335

Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
 340 345 350

Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
 355 360 365

Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
 370 375 380

Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
 385 390 395 400

Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
 405 410 415

Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
 420 425 430

Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
435 440 445

Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
450 455 460

Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
465 470 475 480

Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
485 490 495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
500 505 510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
515 520 525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
530 535 540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545 550 555 560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
565 570 575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
580 585 590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
595 600 605

Lys Gly Ile Leu Ala Thr Ile Glu Gln Phe Cys Ala
610 615 620

<210> 7

<211> 1182

<212> DNA

<213> Methylomonas 16a

<400> 7

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gttgccaggc atccggataa atatcaagtc gttgcgctga ccgccaacgg caatatcgac 120

gcattgtatg aacaatgcct ggcccacat ccggagtatg cggtggtggt catggaaagc 180

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gtatctgtcg gcgcggccgg attgttgccg accttgcccg cggccaaggc cgcaaaaacc      360
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gccagtttta aaccggagca tgccggcagc ctcgcaattgg ttttgaggcg cgatcaagat     1140
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<213> Methylomonas 16a
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20            25            30

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Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
35            40            45

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His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
50            55            60

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Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65            70            75            80

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Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
 85 90 95

Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
 100 105 110

Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
 115 120 125

Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
 130 135 140

Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
 145 150 155 160

Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
 165 170 175

Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
 180 185 190

Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
 195 200 205

Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
 210 215 220

Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
 225 230 235 240

Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
 245 250 255

Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
 260 265 270

Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
 275 280 285

Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
 290 295 300

Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala
 305 310 315 320

Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu
 325 330 335

Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile
 340 345 350

Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
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Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
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<211> 693

<212> DNA

<213> Methylobionas 16a

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gacccttatt ggctgaact gtccatagcc aaacacccc acatcatcac cgcgcctggc 240

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gaaaatgatt ggggtgctgt acacgacgcc gcccgccct gcttgacggg cagcgacatc 360

caccttcaaa tcgatacctt aaaaaatgac ccggtcgggc gcactctggc cttgagttcg 420

cacgacacat tgaacacagt ggatgggtgac acgatcaccg caacataga cagaaagcac 480

gtctggcgcg ccttgacgcc gcaaatgttc aaatacggca tgttgcgga cgcgttgcaa 540

cgaaccgaag gcaatccggc cgtcaccgac gaagccagtg cgctggaact ttggggccat 600

aaaccacaaa tcgtggaagg ccgcccggac aacatcaaaa tcaccggccc ggaagatttg 660

gccctggcac aattttatat ggagcaacaa gca 693

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<211> 231

<212> PRT

<213> Methylobionas 16a

<400> 10

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20 25 30

Gly Lys Thr Val Ile Glu His Thr Leu Thr Arg Leu Leu Glu Ser Asp
35 40 45

Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp
50 55 60

Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly
65 70 75 80

Gly Lys Glu Arg Ala Asp Ser Val Leu Ser Ala Leu Lys Ala Leu Glu
85 90 95

Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg
100 105 110

Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys
115 120 125

Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu
130 135 140

Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His
145 150 155 160

Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg
165 170 175

Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala
180 185 190

Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg
195 200 205

Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln
210 215 220

Phe Tyr Met Glu Gln Gln Ala
225 230

<210> 11
 <211> 855
 <212> DNA
 <213> Methylobionas 16a

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 <212> PRT
 <213> Methylobionas 16a

<400> 12

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 20 25 30

Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr
 35 40 45

Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser
 50 55 60

Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu
65 70 75 80

Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys
85 90 95

Asn Leu Pro Met Gly Gly Gly Leu Gly Gly Gly Ser Ser Asp Ala Ala
100 105 110

Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys
115 120 125

Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val
130 135 140

Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu
145 150 155 160

Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp
165 170 175

Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg
180 185 190

Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg
195 200 205

Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp
210 215 220

Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr
225 230 235 240

Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser
245 250 255

Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly
260 265 270

Leu Asn Gln Ser Ala Leu Tyr Lys Lys Leu Glu Gln Gly
275 280 285

<210> 13
<211> 471

<212> DNA
 <213> Methylomonas 16a

<400> 13
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 gtgtgcacg cattggccga cgccatcttg ggagccgcg ctttgggcga catcggaaca 180
 catttcccg acaccgacc caatttcaag ggccgcgaca gcagggtgct actgcgccac 240
 gtgtacggca tcgtcaagga aaaaggctat aaactggtca acgccgacgt gaccatcatc 300
 gtcaggcgc cgaagatgct gccacacgtg cccggcatgc gcgccaacat tgcgcgccat 360
 ctggaaacgg atgtcgattt cattaatgta aaagccacga cgaccgagaa actgggcttt 420
 gagggcgta aggaaggcat cgccgtgcag gctgtggtgt tgatagaacg c 471

<210> 14
 <211> 157
 <212> PRT
 <213> Methylomonas 16a

<400> 14

Met Ile Arg Val Gly Met Gly Tyr Asp Val His Arg Phe Asn Asp Gly
 1 5 10 15

Asp His Ile Ile Leu Gly Gly Val Lys Ile Pro Tyr Glu Lys Gly Leu
 20 25 30

Glu Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Ala Asp Ala
 35 40 45

Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp
 50 55 60

Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His
 65 70 75 80

Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp
 85 90 95

Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly
 100 105 110

Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile
 115 120 125

Asn Val Lys Ala Thr Thr Thr Glu Lys Leu Gly Phe Glu Gly Arg Lys
130 135 140

Glu Gly Ile Ala Val Gln Ala Val Val Leu Ile Glu Arg
145 150 155

<210> 15
<211> 1632
<212> DNA
<213> Methylobionas 16a

<400> 15
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gatccctaca tcaacgtcga ccccggcacc atgagcccggt tcaaacacgg cgaggtgttc 180
gtgaccgaag acggtgcga aaccgatttg gaccttggcc attacgaacg gtttttgaag 240
accacgatga ccaagaaaaa caacttcacc accggtcagg ttacaggaac ggtattacgc 300
aacgagcgca aaggtgatta tcttggcgcg accgtgcaag tcattccaca tatcacggac 360
gaaatcaaac gccgggtgta tgaagcgcc gaagggaag atgtggcatt gatcgaagtc 420
ggcggcacgg tggcgacat cgaatcgta ccgtttctgg aaaccatacg ccagatgggc 480
gtggaactgg gtcgtgaccg cgccttggtc attcatttga cgtgtgtgac ttacatcaaa 540
tcggcgcgcg aactgaaaac caagcccacc cagcattcgg tcaagaacct gcgcaccatc 600
gggattcagc cggacatttt gatctgtcgt tcagaacaac cgatcccggc cagtgaacgc 660
cgcaagatcg cgctatttac caatgtcgcc gaaaaggcgg tgatttccgc gatcgatgcc 720
gacaccattt accgcattcc gctattgctg cgcgaacaag gcctggacga cctggtggtc 780
gatcagttgc gcctggacgt accagcgcg gatttatcgg cctgggaaaa ggtcgtcgat 840
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accgaattcc tgccgaaatc gccacaccct gtgatcggtg tgatcaccga atggatggac 1260
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ggcgcgcaaa aatgccgcct gaaggctgat tccttggcct ttcagttgta tcaaaaagac 1380

gtcatcacgc agcgtcacgc ccacgcgtac gaattcaaca atcaatatatt aaaacaactg 1440
 gaagcggcgc gcatgaaatt ttccggtaaa tcgctggacg gccgcctggt ggagatcatc 1500
 gagctaccgc aacacccctg gttcctggcc tgccagttcc atcccggaatt cacctcgacg 1560
 ccgcgtaacg gccacgcctt attttcgggc ttcgtcgaag cggccgcca acacaaaaa 1620
 caaggcacag ca 1632

<210> 16
 <211> 544
 <212> PRT
 <213> Methylomonas 16a

<400> 16

Met Thr Lys Phe Ile Phe Ile Thr Gly Gly Val Val Ser Ser Leu Gly
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Lys Gly Ile Ala Ala Ser Ser Leu Ala Ala Ile Leu Glu Asp Arg Gly
 20 25 30

Leu Lys Val Thr Ile Thr Lys Leu Asp Pro Tyr Ile Asn Val Asp Pro
 35 40 45

Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp
 50 55 60

Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys
 65 70 75 80

Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu
 85 90 95

Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val
 100 105 110

Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu
 115 120 125

Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Gly Thr Val
 130 135 140

Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly
 145 150 155 160

Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val
 165 170 175

Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His
 180 185 190

Ser Val Lys Glu Leu Arg Thr Ile Gly Ile Gln Pro Asp Ile Leu Ile
 195 200 205

Cys Arg Ser Glu Gln Pro Ile Pro Ala Ser Glu Arg Arg Lys Ile Ala
 210 215 220

Leu Phe Thr Asn Val Ala Glu Lys Ala Val Ile Ser Ala Ile Asp Ala
 225 230 235 240

Asp Thr Ile Tyr Arg Ile Pro Leu Leu Leu Arg Glu Gln Gly Leu Asp
 245 250 255

Asp Leu Val Val Asp Gln Leu Arg Leu Asp Val Pro Ala Ala Asp Leu
 260 265 270

Ser Ala Trp Glu Lys Val Val Asp Gly Leu Thr His Pro Thr Asp Glu
 275 280 285

Val Ser Ile Ala Ile Val Gly Lys Tyr Val Asp His Thr Asp Ala Tyr
 290 295 300

Lys Ser Leu Asn Glu Ala Leu Ile His Ala Gly Ile His Thr Arg His
 305 310 315 320

Lys Val Gln Ile Ser Tyr Ile Asp Ser Glu Thr Ile Glu Ala Glu Gly
 325 330 335

Thr Ala Lys Leu Lys Asn Val Asp Ala Ile Leu Val Pro Gly Gly Phe
 340 345 350

Gly Glu Arg Gly Val Glu Gly Lys Ile Ser Thr Val Arg Phe Ala Arg
 355 360 365

Glu Asn Lys Ile Pro Tyr Leu Gly Ile Cys Leu Gly Met Gln Ser Ala
 370 375 380

Val Ile Glu Phe Ala Arg Asn Val Val Gly Leu Glu Gly Ala His Ser
 385 390 395 400

Thr Glu Phe Leu Pro Lys Ser Pro His Pro Val Ile Gly Leu Ile Thr
 405 410 415

Glu Trp Met Asp Glu Ala Gly Glu Leu Val Thr Arg Asp Glu Asp Ser
420 425 430

Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Gln Lys Cys Arg Leu Lys
435 440 445

Ala Asp Ser Leu Ala Phe Gln Leu Tyr Gln Lys Asp Val Ile Thr Glu
450 455 460

Arg His Arg His Arg Tyr Glu Phe Asn Asn Gln Tyr Leu Lys Gln Leu
465 470 475 480

Glu Ala Ala Gly Met Lys Phe Ser Gly Lys Ser Leu Asp Gly Arg Leu
485 490 495

Val Glu Ile Ile Glu Leu Pro Glu His Pro Trp Phe Leu Ala Cys Gln
500 505 510

Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe
515 520 525

Ser Gly Phe Val Glu Ala Ala Ala Lys His Lys Thr Gln Gly Thr Ala
530 535 540

<210> 17

<211> 954

<212> DNA

<213> Methylobionas 16a

<400> 17

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cataaccgca ccgtgggtcga tggactgaaa caaaaagggtg cgggtgttcac cgaggaaacta	180
agcgtatgtc cggtgggttc ctacttgatt ttcagcgcgc acggcgtatc caaggagggtg	240
caacaggaag ccgaggagcg ccagttgacg gtattcgatg cgacttgacc gctggtgacc	300
aaagtgcaca tgcaggttgc caagcatgcc aaacaggggc gagaagtgat ttgatcggc	360
cacgcccgtc atccggaagt ggaaggcacg atgggcacgt atgaaaaatg caccgaaggc	420
ggcggcattt atctgggtcga aactccggaa gacgtacgca atttgaaagt caacaatccc	480
aatgatctgg cctatgtgac gcagacgacc ttgtcgatga ccgacaccaa ggatcgggtg	540
gatgcgttac gcgaacaatt tccgtccatt aaggagcaaa aaaaggacga tatttggtaa	600

gagacgcaaa accgtcagga tgcggtgcat gatctggcca agatttcoga cctgattctg 660
gttgctgctt ctccaatag ttccaattcc aaccgtttgc gtgaaatcgc cgtgcaactc 720
ggtaaaccccg cttatttgat cgatacttac caggatttga agcaagattg gctggaggga 780
attgaagtag tcgggggttac cgcgggcgct tcggcgcccg aagtgttggt gcaggaagtg 840
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gaggaaaaagg tagtcttttc gattccaag gagttgaaaa aacatatgca agcg 954

<210> 18
<211> 318
<212> PRT
<213> Methylomonas 16a

<400> 18

Met Gln Ile Val Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp
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Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro
20 25 30

Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly
35 40 45

Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro
50 55 60

Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val
65 70 75 80

Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
85 90 95

Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
100 105 110

Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
115 120 125

Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Ile Tyr
130 135 140

Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro
145 150 155 160

Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr
165 170 175

Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu
180 185 190

Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala
195 200 205

Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser
210 215 220

Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu
225 230 235 240

Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp
245 250 255

Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala
260 265 270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly
275 280 285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val
290 295 300

Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala
305 310 315

<210> 19
<211> 891
<212> DNA
<213> Methylobionas 16a

<400> 19
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gtattgaacg gcggcaaacg caccggcccc ttgttgactt atgcgaccgg tcaggetttg 180
ggcttgcggg aaaacgtgct ggatgcgcgc gcttgcgcgg tagaattcoat coatgtgtat 240
tcgctgattc acgacgatct gccggccatg gacaacgatg atctgcgcgc cggcaaacgc 300
acctgtcaca aggccttacga cgaggccacc gccattttg ccggcgacgc actgcaggcg 360
ctggcctttg aagttctggc caacgacccc ggcatcaccg tcgatgcccc ggctegcctg 420

aaaatgatca cggttttgac cgcgccagc ggctctcaag gcatggtggg cggtaagcc 480
 atcgcgtctcg gctccgtcgg ccgcaaatg acgctgcggg aactcgaaaa catgcatac 540
 cacaagactg gcgcctgat ccgcgccagc gtcaatctgg cggcattatc caaaccggat 600
 ctggatactt gcgtgcgcaa gaaactggat cactatgcca aatgcatagg cttgtcgttc 660
 caggtcaaa acgacattct cgacatcgaa gccgacaccg cgacactcgg caagactcag 720
 ggcaaggaca tcgataacga caaaccgacc tacctgcgc tattgggcat ggctggcgcc 780
 aaacaaaaa cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc 840
 gaagccgacc tgctgcgcga actatcgctt tacatcatcg agcgacgcga c 891

<210> 20
 <211> 297
 <212> PRT
 <213> Methylomonas 16a

<400> 20

Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu
1 5 10 15

Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr
20 25 30

Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr
35 40 45

Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu
50 55 60

Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr
65 70 75 80

Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg
85 90 95

Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile
100 105 110

Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn
115 120 125

Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr
130 135 140

Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gly Gln Ala
145 150 155 160

Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu
165 170 175

Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn
180 185 190

Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys
195 200 205

Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp
210 215 220

Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln
225 230 235 240

Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly
245 250 255

Met Ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val
260 265 270

Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu
275 280 285

Ser Leu Tyr Ile Ile Glu Arg Thr His
290 295

<210> 21
<211> 1533
<212> DNA
<213> Methylomonas 16a

<400> 21
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ggccgcaacc gccgatcaa catgaacggc ttaccttcg ataccggtcc gacattcttg 180
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gtctattccg acgcgagaa catgcgcgcc gaattgcaac gggatttcga cgaagcgacg 360
gacggctacg aacagtctcat ggaacaggaa cgaaacgct tcaacgcgct gtatccctgc 420

atcacccgcg attattccag cctgaaatcc tttttgtcgc tggacttgat caaggccctg 480
 ccgtggctgg cttttccgaa aagcgtgttc aataatctcg gccagtattt caaccaggaa 540
 aaaatgcgcc tggccttttg ctttcagtcc aagtatctgg gcatgtgcgc gtgggaatgc 600
 ccggcactgt ttacgatgct gccctatctg gagcacgaat acggcattta tcacgtcaaa 660
 ggcggcctga accgcatcgc ggcggcgatg gcgcaagtga tcgcggaaaa cggcggcgaa 720
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 aattgctatc tggtcggcgg cggcacgcat cccggtagcg gtttgccgac catctacgaa 1440
 tcggcgcgga tttcggccaa gctgatttcc cagaaacatc gggtgaggtt caaggacata 1500
 gcacacagcg cctggctgaa aaaagccaaa gcc 1533

<210> 22
 <211> 511
 <212> PRT
 <213> *Methylobionas* 16a

<400> 22

Met Ala Asn Thr Lys His Ile Ile Ile Val Gly Ala Gly Pro Gly Gly
 1 5 10 15

Leu Cys Ala Gly Met Leu Leu Ser Gln Arg Gly Phe Lys Val Ser Ile
 20 25 30

Phe Asp Lys His Ala Glu Ile Gly Gly Arg Asn Arg Pro Ile Asn Met
 35 40 45

Asn Gly Phe Thr Phe Asp Thr Gly Pro Thr Phe Leu Leu Met Lys Gly
 50 55 60

Val Leu Asp Glu Met Phe Glu Leu Cys Glu Arg Arg Ser Glu Asp Tyr
65 70 75 80

Leu Glu Phe Leu Pro Leu Ser Pro Met Tyr Arg Leu Leu Tyr Asp Asp
85 90 95

Arg Asp Ile Phe Val Tyr Ser Asp Arg Glu Asn Met Arg Ala Glu Leu
100 105 110

Gln Arg Val Phe Asp Glu Gly Thr Asp Gly Tyr Glu Gln Phe Met Glu
115 120 125

Gln Glu Arg Lys Arg Phe Asn Ala Leu Tyr Pro Cys Ile Thr Arg Asp
130 135 140

Tyr Ser Ser Leu Lys Ser Phe Leu Ser Leu Asp Leu Ile Lys Ala Leu
145 150 155 160

Pro Trp Leu Ala Phe Pro Lys Ser Val Phe Asn Asn Leu Gly Gln Tyr
165 170 175

Phe Asn Gln Glu Lys Met Arg Leu Ala Phe Cys Phe Gln Ser Lys Tyr
180 185 190

Leu Gly Met Ser Pro Trp Glu Cys Pro Ala Leu Phe Thr Met Leu Pro
195 200 205

Tyr Leu Glu His Glu Tyr Gly Ile Tyr His Val Lys Gly Gly Leu Asn
210 215 220

Arg Ile Ala Ala Ala Met Ala Gln Val Ile Ala Glu Asn Gly Gly Glu
225 230 235 240

Ile His Leu Asn Ser Glu Ile Glu Ser Leu Ile Ile Glu Asn Gly Ala
245 250 255

Ala Lys Gly Val Lys Leu Gln His Gly Ala Glu Leu Arg Gly Asp Glu
260 265 270

Val Ile Ile Asn Ala Asp Phe Ala His Ala Met Thr His Leu Val Lys
275 280 285

Pro Gly Val Leu Lys Lys Tyr Thr Pro Glu Asn Leu Lys Gln Arg Glu
290 295 300

Tyr Ser Cys Ser Thr Phe Met Leu Tyr Leu Gly Leu Asp Lys Ile Tyr
305 310 315 320

Asp Leu Pro His His Thr Ile Val Phe Ala Lys Asp Tyr Thr Thr Asn
325 330 335

Ile Arg Asn Ile Phe Asp Asn Lys Thr Leu Thr Asp Asp Phe Ser Phe
340 345 350

Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly
355 360 365

Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly
370 375 380

Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp
385 390 395 400

Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu
405 410 415

Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val
420 425 430

Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu
435 440 445

Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu
450 455 460

Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu
465 470 475 480

Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg
485 490 495

Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala
500 505 510

<210> 23
<211> 1491
<212> DNA
<213> Methylobionas 16a

<400> 23
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gtcggcgcca agctcaacat catgacaaa gacggcttta ccttcgatct ggggcccgtcc 180
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gatcgggat tcaaaagcca tcgcctgtcg gacgatccga ccatttatct ggtcgcgccg 1080
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cgggtgtcgg taaaactcga acgcatgggc ctgacggatt taegccaaca catcgtgacc 1260
gaagaatact ggacgccgct ggatattcag gccaaatatt attcaaacca gggctcgatt 1320
tacggcgtg tcgcgcaccg cttcaaaaac ctgggtttca aggcacctca acgcagcagc 1380
gaattattcca atctgtatct cgtcggcgcc agcgtcaatc ccggcgcgcg catgcgcgat 1440
gtgacgctgt ccgggcaatt ggtgagggac aagattgtgg cggatttgca a 1491

<210> 24
<211> 497
<212> PRT
<213> Methylobionas 16a

<400> 24

Met Asn Ser Asn Asp Asn Gln Arg Val Ile Val Ile Gly Ala Gly Leu
1 5 10 15

Gly Gly Leu Ser Ala Ala Ile Ser Leu Ala Thr Ala Gly Phe Ser Val
20 25 30

Gln Leu Ile Glu Lys Asn Asp Lys Val Gly Gly Lys Leu Asn Ile Met
35 40 45

Thr Lys Asp Gly Phe Thr Phe Asp Leu Gly Pro Ser Ile Leu Thr Met
50 55 60

Pro His Ile Phe Glu Ala Leu Phe Thr Gly Ala Gly Lys Asn Met Ala
65 70 75 80

Asp Tyr Val Gln Ile Gln Lys Val Glu Pro His Trp Arg Asn Phe Phe
85 90 95

Glu Asp Gly Ser Val Ile Asp Leu Cys Glu Asp Ala Glu Thr Gln Arg
100 105 110

Arg Glu Leu Asp Lys Leu Gly Pro Gly Thr Tyr Ala Gln Phe Gln Arg
115 120 125

Phe Leu Asp Tyr Ser Lys Asn Leu Cys Thr Glu Thr Glu Ala Gly Tyr
130 135 140

Phe Ala Lys Gly Leu Asp Gly Phe Trp Asp Leu Leu Lys Phe Tyr Gly
145 150 155 160

Pro Leu Arg Ser Leu Leu Ser Phe Asp Val Phe Arg Ser Met Asp Gln
165 170 175

Gly Val Arg Arg Phe Ile Ser Asp Pro Lys Leu Val Glu Ile Leu Asn
180 185 190

Tyr Phe Ile Lys Tyr Val Gly Ser Ser Pro Tyr Asp Ala Pro Ala Leu
195 200 205

Met Asn Leu Leu Pro Tyr Ile Gln Tyr His Tyr Gly Leu Trp Tyr Val
210 215 220

Lys Gly Gly Met Tyr Gly Met Ala Gln Ala Met Glu Lys Leu Ala Val
225 230 235 240

Glu Leu Gly Val Glu Ile Arg Leu Asp Ala Glu Val Ser Glu Ile Gln
245 250 255

Lys Gln Asp Gly Arg Ala Cys Ala Val Lys Leu Ala Asn Gly Asp Val
260 265 270

Leu Pro Ala Asp Ile Val Val Ser Asn Met Glu Val Ile Pro Ala Met
275 280 285

Glu Lys Leu Leu Arg Ser Pro Ala Ser Glu Leu Lys Lys Met Gln Arg
290 295 300

Phe Glu Pro Ser Cys Ser Gly Leu Val Leu His Leu Gly Val Asp Arg
305 310 315 320

Leu Tyr Pro Gln Leu Ala His His Asn Phe Phe Tyr Ser Asp His Pro
325 330 335

Arg Glu His Phe Asp Ala Val Phe Lys Ser His Arg Leu Ser Asp Asp
340 345 350

Pro Thr Ile Tyr Leu Val Ala Pro Cys Lys Thr Asp Pro Ala Gln Ala
355 360 365

Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu
370 375 380

Asp Pro Asp Lys Leu Leu Thr Ala Glu Asp Tyr Ser Ala Leu Arg Glu
385 390 395 400

Arg Val Leu Val Lys Leu Glu Arg Met Gly Leu Thr Asp Leu Arg Gln
405 410 415

His Ile Val Thr Glu Glu Tyr Trp Thr Pro Leu Asp Ile Gln Ala Lys
420 425 430

Tyr Tyr Ser Asn Gln Gly Ser Ile Tyr Gly Val Val Ala Asp Arg Phe
435 440 445

Lys Asn Leu Gly Phe Lys Ala Pro Gln Arg Ser Ser Glu Leu Ser Asn
450 455 460

Leu Tyr Phe Val Gly Gly Ser Val Asn Pro Gly Gly Gly Met Pro Met
465 470 475 480

Val Thr Leu Ser Gly Gln Leu Val Arg Asp Lys Ile Val Ala Asp Leu
485 490 495

Gln

<210> 25
<211> 912
<212> DNA
<213> Pantoea stewartii

<400> 25
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gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgtc 660
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gcgcgtcagtt aa 912

<210> 26
<211> 303
<212> PRT
<213> Pantoea stewartii

<400> 26

Leu Thr Val Cys Ala Lys Lys His Val His Leu Thr Gly Ile Ser Ala
1 5 10 15

Glu Gln Leu Leu Ala Asp Ile Asp Ser Arg Leu Asp Gln Leu Leu Pro
20 25 30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
35 40 45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Thr Ala
50 55 60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65 70 75 80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
85 90 95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
100 105 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
115 120 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
130 135 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145 150 155 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
165 170 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
180 185 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
195 200 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
210 215 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225 230 235 240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
245 250 255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
260 265 270

Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
275 280 285

Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
290 295 300

<210> 27

<211> 1296

<212> DNA

<213> *Pantoea stewartii*

<400> 27

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aaagcgctgg taacgggcag cgatatcgga ttccagacgc tcggactgca aacgcatact   180
cccggttctc tatcgacact gctgcacctg gccgcgcacc cactcggacc ctcgatgtta   240
cgactgatca atgaaatggc acgtaccagc gatatgcttt gccgggaact gcccgccgct   300
tttcatgcgt tgcagataga gggcgtgata gttgatcaaa tggagccggc aggtgcagta   360
gtcgcagaag cgtcaggctc gccgtttgtt tcggtggcct gccgcgtgcc gctcaaccgc   420
gaacggggtt tgccctctggc ggtgatgcct ttcgagtaac gcaccagcga tgcggctcgg   480
gaacgctata ccaccagcga aaaaatttat gactggctga tgcgaagtcg cgatcgtgtg   540
atcgcgcata atgcatacag aatgggttta gccccgcgtg aaaaactgca tcattgtttt   600
tctccactgg cacaatcag ccagttgatc cccgaactgg attttcccg caaagcgtcg   660
ccagactgct ttcatacggt tggaccgtta cggcaacccc aggggaagcc ggggtcatca   720
actttatttt ttcctcccc ggacaaaccc cgtatttttg cctcgtctgg caccctgcag   780
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atcgccaagc gtgcgtctcg gtttactacc agccatgcgc tggcgcgcca gattcgatcg  1140
ctgtcgacta acaccgatta cccgcagcgt atgacaaaaa ttcaggccgc attgcgtctg  1200

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gtactcagtg ggcaggatta tgcaaccgca ctatga 1296

<210> 28
<211> 431
<212> PRT
<213> Pantoea stewartii

<400> 28

Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg
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Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
20 25 30

Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
35 40 45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
50 55 60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65 70 75 80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
85 90 95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
100 105 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
115 120 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
130 135 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145 150 155 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
165 170 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
180 185 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
 195 200 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
 210 215 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
 225 230 235 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
 245 250 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
 260 265 270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
 275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
 290 295 300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
 305 310 315 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
 325 330 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
 340 345 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
 355 360 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
 370 375 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
 385 390 395 400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
 405 410 415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
 420 425 430

<210> 29
 <211> 1149
 <212> DNA
 <213> *Pantoea stewartii*

<400> 29
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 tacacgcctg attctgcact acgcgtagga ttccaggcat ttatcggtca ggagtggcaa 480
 ctgagcgcgc cgcattggtt atcgtcaccg attatcatgt atgcgacggt cgatcagcaa 540
 aatggctacc gctttgttta taccctgccg ctttccgcaa ccgactgctg gatcgaagac 600
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 tatgctgcgc gacagggttg gcctttacag acgttgcctg gggagaagaa ggggtgcattg 720
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<210> 30
 <211> 382
 <212> PRT
 <213> *Pantoea stewartii*

<400> 30

Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn
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Gly Leu Ile Ala Leu Arg Leu Gln Gln His Pro Asp Met Arg Ile
 20 25 30

Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
35 40 45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
195 200 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
210 215 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225 230 235 240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Pro
245 250 255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
260 265 270

Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
275 280 285

Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
290 295 300

Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305 310 315 320

Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
325 330 335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
340 345 350

Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
355 360 365

Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
370 375 380

<210> 31

<211> 1479

<212> DNA

<213> Pantoea stewartii

<400> 31

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tatgtttatc aggagcaggg ctttactttt gatgcaggcc ctaccgttat caccgatccc	180
agcgcgattg aagaactggt tgctctggcc ggtaaacagc ttaaggatta cgtcgagctg	240
ttgcgggtca cgccgtttta tcgcctgtgc tgggagtcgc gcaaggctct caattacgat	300
aacgaccagg ccaggttaga agcgcagata cagcagttta atccgcgcga tgttgccgggt	360
tatcgagcgt tccttgacta ttgcggtgcc gtattcaatg agggctatct gaagctcggc	420
actgtgcctt ttttatcggt caaagacatg ctteggggccg cgccccgatt ggcaagcgtg	480
caggcatggc gcagcggtta cagtaaaagt gccgggtaca ttgaggatga gcattctcgg	540
caggcggttt cttttcactc gctcttagtg ggggggaatc cgtttgcaac ctogtcatt	600
tatacgctga ttcacgcgtt agaacgggaa tggggcgctc ggtttccacg cgggtggaacc	660
ggtgcgctg tcaatggcat gatcaagctg ttocaggatc tgggcggcga agtcgtgctt	720

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<210> 32
 <211> 492
 <212> PRT
 <213> Pantoea stewartii
 <400> 32

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Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
 35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
 65 70 75 80

Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95

Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
 100 105 110

Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
115 120 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
130 135 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
210 215 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
245 250 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
275 280 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305 310 315 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
325 330 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
340 345 350

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
370 375 380

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385 390 395 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
405 410 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
435 440 445

Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
450 455 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
485 490

<210> 33
<211> 891
<212> DNA
<213> Pantoea stewartii

<400> 33
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ctggcacaat tacccttacg ctccggcctgg gccatcgaga cagcgaagca ggtgtaccgt 720
aaaattggcg tgaaagtga acaggccggt aagcaggcct gggatcatcg ccagtccacg 780
tccaccgcgg aaaaattaac gcttttgcg acggcatccg gtcaggcagt tacttcccg 840
atgaagacgt atccaccocg tctgtctcat ctctggcagc gcccgatcta g 891

<210> 34
<211> 296
<212> PRT
<213> Pantoea stewartii

<400> 34

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
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Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
35 40 45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Leu Glu Met Lys
50 55 60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
100 105 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
165 170 175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
195 200 205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
245 250 255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
260 265 270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
275 280 285

Ala His Leu Trp Gln Arg Pro Ile
290 295

<210> 35

<211> 528

<212> DNA

<213> Pantoea stewartii

<400> 35

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catgaaccgc gtaaaggcgc atttgaagtt aacgatctct atgccgtggt attcgccatt 180

gtgtcgattg ccttgattta cttcggcagt acaggaaatct ggccgctcca gtggattggt 240

gcaggcatga ccgcttatgg ttactgtat tttatggacc acgacggact ggtacaccag 300

cgctggcgct tccgtacat acgcgcgaaa ggctacctga aacgggtata catggccac 360

cgtatgcac atcgtgtaag gggaaaagag ggctgcgtgt cctttggttt tctgtacgcg 420

ccaccgttat ctaaacttca gccgacgctg agagaaaggc atcgcgctag atcgggcgct 480
gccagagatg agcaggacgg ggtggatacg tottcatccg ggaagtaa 528

<210> 36
<211> 175
<212> PRT
<213> Pantoea stewartii

<400> 36

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1 5 10 15

Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
165 170 175

<210> 37
<211> 1599
<212> DNA
<213> Rhodococcus erythropolis AN12

<400> 37
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 gcgtatctcg cactgtaggg ttggtcggtc gaggttctcg agaaggacac ggttctcgcc 120
 ggtgccgtct cgaccgtcga gcgatttccc ggatacaagg tggaccgggg gtcgtctcgc 180
 cacctcatga tccgacacag tggcatcacc gaggaactcg gactcggcgc gcacggccctt 240
 cgtacatcg actgtgaccc gtggcggttc gtcgcgcccg cccctggcac cgacggggccg 300
 ggcatcgtgt ttcatcgca cctcgatgca acctgccagt ccatagaacg agcttcgggg 360
 acaaggacg ccgacgcgta ccggcggttc gtcgcggtct ggtcggagcg cagccgacac 420
 gtgatgaagg cattttccac accgccacc ggatcgaaac tgatcggtgc gtcggagga 480
 ctggccacag cgcgcggcaa cagcgaactg tcgcggcagt tccctcgccc gggcgacgca 540
 ctgctggagc agtatttoga cagtggagca ctcaaggcag cgttgccgtg gtcggcgcc 600
 cagtcgggcg ctccgatgc ggaaccggga accgctccga tggtcggctt cgcggccctc 660
 atgcacgtcc tgcgcgccg gcgagcagtc ggaggagcg gcgcactgag tgcgtcggtt 720
 gcaccccgga tggctgtcga cggcgccacc gtcgcgctcg gtgacggcgt gacgtcgatc 780
 cgcgggaact cgaatcactg gaccgtcaca accgagagcg gtcgagaagt tcacgtcgc 840
 aaggtaatcg cgggttgcca catcctcacc aactcgatc tccctgggcaa cggaggcttc 900
 gaccgaacca cgtcgtatca ctggcgccgg aagatcaggg tcggcccccg catcgcgct 960
 gtattcgac tggcgacatc tgcgtcccg tccatccgcg gcgacgccac gacacgggaa 1020
 agtacctcgg gattgcaatt actcgtttcc gatcgcgcc acttgcgac tgcacacggc 1080
 gcacactcgg caggggaact gcctcctcgc cctcggttc tcggaatgag ttacagcgga 1140
 atcgatccca cgtcgcgcc ggccggcgcg catcaggtga cactgtgttc gcagtggcag 1200
 ccgtatcgtc tcagcggaca tcgcgattgg cgtcgggtc ccgagggcga ggcgacggg 1260
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 attcaaacct cccgcgacat cgagtcggaa ttggggatga tcggcggaata tgcattgcac 1380
 gtogagatgt cactcgatca gatgatgtt tggcgaccgc tcccgaaact gtccggccat 1440
 cgcgttcggg gagcagacgg gttgtatctg accggagcct cgacgcaccc cggtggtggt 1500
 gtgtccggag ccagtggtcg cagtgcgcgt cgaatcgcac tgtccgacag ccgcgggggt 1560
 aaagcgagtc agtggtatgc tcgttcgagc aggtcgtga 1599

<210> 38
 <211> 532

<212> PRT
<213> Rhodococcus erythropolis AN12

<400> 38

Met Ser Ala Phe Leu Asp Ala Val Val Val Gly Ser Gly His Asn Ala
1 5 10 15

Leu Val Ser Ala Ala Tyr Leu Ala Arg Glu Gly Trp Ser Val Glu Val
20 25 30

Leu Glu Lys Asp Thr Val Leu Gly Gly Ala Val Ser Thr Val Glu Arg
35 40 45

Phe Pro Gly Tyr Lys Val Asp Arg Gly Ser Ser Ala His Leu Met Ile
50 55 60

Arg His Ser Gly Ile Ile Glu Glu Leu Gly Leu Gly Ala His Gly Leu
65 70 75 80

Arg Tyr Ile Asp Cys Asp Pro Trp Ala Phe Ala Pro Pro Ala Pro Gly
85 90 95

Thr Asp Gly Pro Gly Ile Val Phe His Arg Asp Leu Asp Ala Thr Cys
100 105 110

Gln Ser Ile Glu Arg Ala Cys Gly Thr Lys Asp Ala Asp Ala Tyr Arg
115 120 125

Arg Phe Val Ala Val Trp Ser Glu Arg Ser Arg His Val Met Lys Ala
130 135 140

Phe Ser Thr Pro Pro Thr Gly Ser Asn Leu Ile Gly Ala Phe Gly Gly
145 150 155 160

Leu Ala Thr Ala Arg Gly Asn Ser Glu Leu Ser Arg Gln Phe Leu Ala
165 170 175

Pro Gly Asp Ala Leu Leu Asp Glu Tyr Phe Asp Ser Glu Ala Leu Lys
180 185 190

Ala Ala Leu Ala Trp Phe Gly Ala Gln Ser Gly Pro Pro Met Ser Glu
195 200 205

Pro Gly Thr Ala Pro Met Val Gly Phe Ala Ala Leu Met His Val Leu
210 215 220

Pro Pro Gly Arg Ala Val Gly Gly Ser Gly Ala Leu Ser Ala Ala Leu
225 230 235 240

Ala Ser Arg Met Ala Val Asp Gly Ala Thr Val Ala Leu Gly Asp Gly
245 250 255

Val Thr Ser Ile Arg Arg Asn Ser Asn His Trp Thr Val Thr Thr Glu
260 265 270

Ser Gly Arg Glu Val His Ala Arg Lys Val Ile Ala Gly Cys His Ile
275 280 285

Leu Thr Thr Leu Asp Leu Leu Gly Asn Gly Gly Phe Asp Arg Thr Thr
290 295 300

Leu Asp His Trp Arg Arg Lys Ile Arg Val Gly Pro Gly Ile Gly Ala
305 310 315 320

Val Leu Arg Leu Ala Thr Ser Ala Leu Pro Ser Tyr Arg Gly Asp Ala
325 330 335

Thr Thr Arg Glu Ser Thr Ser Gly Leu Gln Leu Leu Val Ser Asp Arg
340 345 350

Ala His Leu Arg Thr Ala His Gly Ala Ala Leu Ala Gly Glu Leu Pro
355 360 365

Pro Arg Pro Ala Val Leu Gly Met Ser Phe Ser Gly Ile Asp Pro Thr
370 375 380

Ile Ala Pro Ala Gly Arg His Gln Val Thr Leu Trp Ser Gln Trp Gln
385 390 395 400

Pro Tyr Arg Leu Ser Gly His Arg Asp Trp Ala Ser Val Ala Glu Ala
405 410 415

Glu Ala Asp Arg Ile Val Gly Glu Met Glu Ala Phe Ala Pro Gly Phe
420 425 430

Thr Asp Ser Val Leu Asp Arg Phe Ile Gln Thr Pro Arg Asp Ile Glu
435 440 445

Ser Glu Leu Gly Met Ile Gly Gly Asn Val Met His Val Glu Met Ser
450 455 460

Leu Asp Gln Met Met Leu Trp Arg Pro Leu Pro Glu Leu Ser Gly His
465 470 475 480

Arg Val Pro Gly Ala Asp Gly Leu Tyr Leu Thr Gly Ala Ser Thr His
485 490 495

Pro Gly Gly Gly Val Ser Gly Ala Ser Gly Arg Ser Ala Ala Arg Ile
500 505 510

Ala Leu Ser Asp Ser Arg Arg Gly Lys Ala Ser Gln Trp Met Arg Arg
515 520 525

Ser Ser Arg Ser
530

<210> 39
<211> 30
<212> DNA
<213> Methylobionas 16a

<400> 39
ccgagtactg aagcgggttt ttgcaggag

30

<210> 40
<211> 25
<212> DNA
<213> Methylobionas 16a

<400> 40
gggctagctg ctccgattgt tacag

25

<210> 41
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer, derived from Rhodococcus erythropolis AN12

<400> 41
agcagctagc ggaggaataa accatgagcg catttctc

38

<210> 42
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer, derived from Rhodococcus erythropolis AN12

<400> 42
gactagtcac gacctgctcg aacgac

26

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 43
atgacggtct gcgcaaaaaa acacg

25

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 44
gagaaattat gttgtggatt tggaatgc

28

<210> 45
<211> 19
<212> DNA
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<220>
<223> primer

<400> 45
gagtttgatc ctggctcag

19

<210> 46
<211> 16
<212> DNA
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<220>
<223> primer

<400> 46
taccttgta cgactt

16

<210> 47
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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 <222> (11)..(11)
 <223> Y = C or T

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> M = A or C

<400> 47
 gtgccagcag ymgcggt 17

<210> 48
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 48
 atgagcgcat ttctcgacg c 21

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 49
 tcacgacctg ctcgaacgac 20

<210> 50
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 50
 gagaattggc tgaaaaacca aataaataac aaaatttagc gagtaaatgg 50

<210> 51
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 51
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<210> 52
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 52
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<210> 53
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 53
 ttaattggtct tgccatgaga tgtgctccga ttgttacagt tatagttata 50

<210> 54
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 54
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<210> 55
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 55
 aaggatccgc gtattcgtac tc 22

<210> 56
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 56
ctggatccga tctagaaata ggctcgagtt gtcgttcagg 40

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 57
aaggatcccta ctcgagctga catcagtgct 30

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 58
gctctagatg caaccagaat cg 22

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 59
tggctcgaga gtaaaacact caag 24

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 60
tagctogagt cacgcttgct 19